```
                        ____________ I ___________                                                          __ II __
human EF2K   122   GEWLDDEVLIKMASQPFGRGAMRECFRTKKLSNFLHAQ--------------------------QWKGASNYVAKRYIEPVD
C. e. EF2K   108   KQWTEDIVDVRLHPDSFARGAMRECYRLKKCSKHGTSQ--------------------------DW--SSNYVAKRYICQVD
MHCK A       570   NKWIRLSMKLKVERKPFAEGALREAYHTVSLGVGTDENYPLGTTTKLFPPIEMISPISKNNEAMTQLKNGTKFVLKLYKKEAE
MHCK B       130   AQWTCTATLVKVEPVPFAEGAFRKAYHTLDLSKSGA----------------------------------SGRYVSKIGKK---
FC-AN09        1         IVCVSIEKTPFAKGSCRTAHKLKDWSQP----------------------------------DQGLVGKFSTNKK-
consensus          **W******o*o****F**G**R**o*******************************************oV*K*******

                         ________________ III ________________                            _____ IV _____
human EF2K   178   ----RDVYFEDVRLQMEAKLWGEEYNRHKPPKQVDIMQMCIIELKDR----PGKPLF-HLEHYIEGKYIKYNSNSGFVRDDNI
C. e. EF2K   162   ----RRVLFDDVRLQMDAKLWAEEYNRYNPPKKIDIVQMCVIEMIDV----KGSPLY-HLEHFIEGKYIKYNSNSGFVSNAA-
MHCK A       653   QQASRELYFEDVKMQMVCRDWGNKFNQKKPPKKIEFLMSWVVELIDRSPSSNGQPILCSIEPLLVGEFKKNNSNYGAVLTN--
MHCK B       177   -PTPRPSYFEDVKMQMIAKKWADKYNSFKPPKKIEFLQSCVLEFVDRTSSD----LICGAEPYVEGQYRKYNNNSGFVSNDE-
FC-AN09       42   --TTRDSYFTDVLMQTFCAKWAEKFNEAKPPKPITFLPSYVYELIDHPPPY---PV-CGGEPFIEGDYKKHNNNSGYVSSDA-
consensus          ****R**oF*DV*oQ*****W***oN***PPK*o*oo***ooEo*D*********o****E*oo*G*o*K*N*N*G*V*****

                    ________________ V ________________________________ VI ______________
human EF2K   252   RLTPQAFSHFTFERSGHQLIVVDIQGVGDLYTDPQIHTETGTDFGDGNLGVRGMALFFYSHACNRICESMGLAPFDLSPRERD
C. e. EF2K   235   RLTPQAFSHFTFERSGHQMMVVDIQGVGDLYTDPQIHTVVGTDYGDGNLGTRGMALFFHSHRCNDICETMDLSNFELSPPEIE
MHCK A       734   RSTPQAFSHFTYELSNKQMIVVDIQGVDDLYTDPQIHTPDGKGFGLGNLGKAGINKFITTHKCNAVCALLDL-DVKLG-----
MHCK B       254   RNTPQSFSHFTYEHSNHQLLIIDIQGVGDHYTDPQIHTYDGVGFGIGNLGQKGFEKFLDTHKCNAICQYLNLQSIN-------
FC-AN09      118   RNTPQSFSHFSYELSNHELLIVDIQGVNDFYTDPQIHTKSGEGFGEGNLGETGFHKFLQTHKCNPVCDFLKLKPIN-------
consensus          R*TPQ*FSHF*oE*S***ooooDIQGV*DoYTDPQIHT**G**oG*GNLG**Go**Fo**H*CN*oC**o*L**o********

                              __ VII __
human EF2K   335   AVNQNTKLLQSAKT--ILRGTEEKCGS
C. e. EF2K   318   ATEVAMEVAAKQKKSCIVPPTVFEARR
MHCK A       811   ----GVLSGNNKKQ--LQQGTMVMPDI
MHCK B       330   --------PKSEKSDC---GTVPRPDL
FC-AN09      194   ---------QSKKA--LLRGTLPVVQL
consensus          ************K*******T******
```

Figure 1A

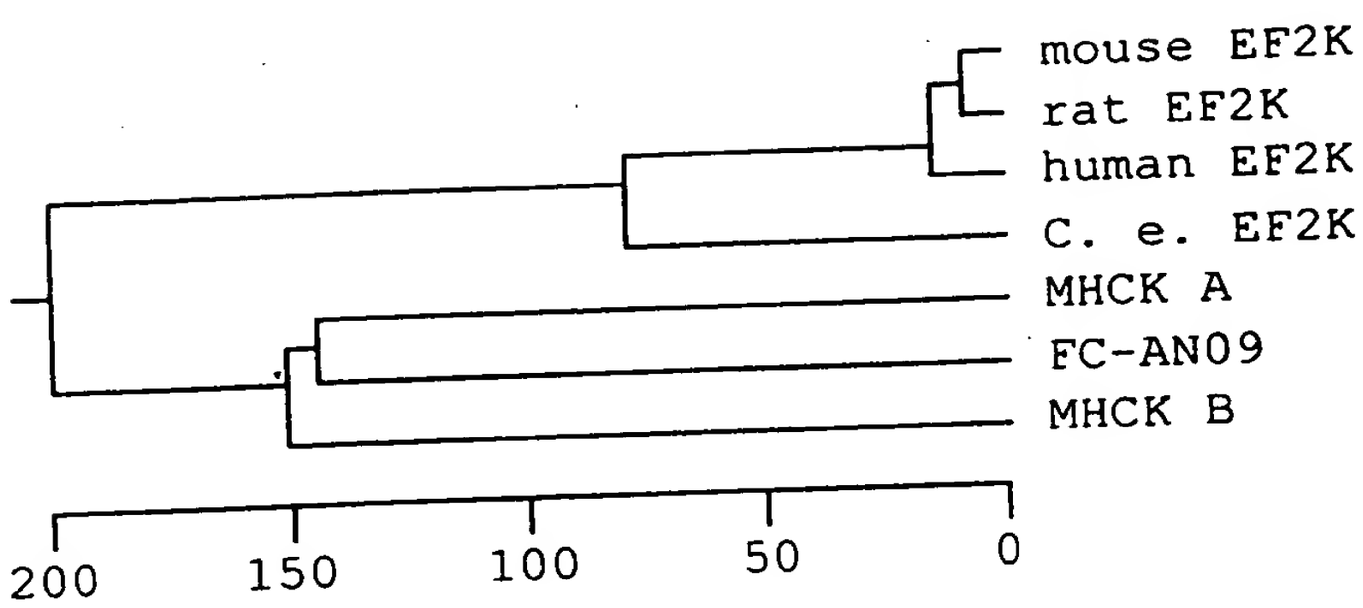

Figure 1B

601-1-098CIP

```
   human eEF-2K   1    .........R.......QSP....DG...G....E...........        44
C. elegans eEF-2K 1    MTIDTTNESDNSPTNSPGLEASARTFSLNASKMVR------ITD          38
   mouse eEF-2K   1    MADEDLIFCLEGVDGGRCSRAGHNADSDTDSDDDEGYFICPITD          44

   human eEF-2K   45   .PS.....N...NK.......S.RY.SS....N.............Q...-   93
C. elegans eEF-2K 39   DYADEVFIEQNDVVIEKPRMD---------PLHVRKLMETWRKAARRART    79
   mouse eEF-2K   45   DHMSNQNVSSKVQSYYSNLTKTECGS-TGSPASSFHFKEAWKHAIEKAK-    92

   human eEF-2K   94   ...................R..............D................   143
C. elegans eEF-2K 80   NYIDPWDEFNIHEYPVQRAKRYRYSAIRKQWTEDIVDVRLHPDSFARGAM    129
   mouse eEF-2K   93   HMPDPWAEFHLEDIATEHATRHRYNAVTGEWLKDEVLIKMASQPFGRGAM    142
         MHCK A   572                                WIRLSMKLKVERKPFAEGAL    591

   human eEF-2K   144  .........------------------------...........          166
C. elegans eEF-2K 130  RECYRLKKCS-------------------------KHGTSQDW--SSN      150
   mouse eEF-2K   143  RECFRTKKLS-------------------------NFLHAQQWKGASN      165
         MHCK A   592  REAYHTVSLGVGTDENYPLGTTTKLFPPIEMISPISKNNEAMTQLKNGTK    641

   human eEF-2K   167  ..........----.D.....R..........E...............      212
C. elegans eEF-2K 151  YVAKRYICQVD----RRVLFDDVRLQMDAKLWAEEYNRYNPPKKIDIVQM    196
   mouse eEF-2K   166  YVAKRYIEPVD----RSVYFEDVQLQMEAKLWGEDYNRHKPPKQVDIMQM    211
         MHCK A   642  FVLKLYKKEAEQQASRELYFEDVKMQMVCRDWGNKFNQKKPPKKIEFLMS    691

   human eEF-2K   213  .........----.K.-......................-....          256
C. elegans eEF-2K 197  CVIEMIDVK----GSP-LYHLEHFIEGKYIKYNSNSGFV-S-NAARLTPQ    239
   mouse eEF-2K   212  CIIELKDRP----GQP-LFHLEHYIEGKYIKYNSNSGFVRDDNI-RLTPQ    255
         MHCK A   692  WVVELIDRSPSSNGQPILCSIEPLLVGEFKKNNSNYGAVLT-N--RSTPQ    738
```

Figure 2A

```
        human eEF-2K  257  .................................T................  306
   C.elegans eEF-2K  240  AFSHFTFERSGHQMMVVDIQGVGDLYTDPQIHTVVGTDYGDNLGTRGMA   289
        mouse eEF-2K  256  AFSHFTFERSGHQLIVVDIQGVGDLYTDPQIHTEKGTDFGDNLGVRGMA   305
             MHCK A  739  AFSHFTYELSNKQMIVVDIQGVDDLYTDPQIHTPDGKGFGLGNLGKAGIN  788

        human eEF-2K  307  ............E....A........R.....N.K.......--......  354
   C.elegans eEF-2K  290  LFFHSHRCNDICETMDLSNFELSPPEIEATEVAMEVAAKQKKSCIVPPTV  339
        mouse eEF-2K  306  LFFYSHACNRICQSMGLTPFDLSPREQDAVNQSTRLLQSAKT--ILRGTE  353
             MHCK A  789  KFITTHKCNAVCALLDL                                  805

        human eEF-2K  355  .......V...G..---.....-RP.........................  400
   C.elegans eEF-2K  340  FEARRNRISSECVHVEHGISMDQLRKRKTL---NQSSTDLSAKSHNEDCV  386
        mouse eEF-2K  354  EKCGSPRIRTLSSS---RPPLL-LRLSENSGDENMSDVTFDSLPSSPSSA  399

        human eEF-2K  401  .........-......S.....AS....HL....E..............G  449
   C.elegans eEF-2K  387  CPECIPVVEQLCEPCSEDEEDEEEDYPRSEKSGNSQKSRRSRMSISTRSS  436
        mouse eEF-2K  400  TPHSQKLDH-LHWPVFGDLDNMGPRDHDRMDNHRDSENSGDSGYPSEKRS  448

        human eEF-2K  450  -E.........--..YS..-KY.........-.......K.....S...  494
   C.elegans eEF-2K  437  GDESASRPRKCGFVDLNSLRQRHDSFRSSVGTYSMNSSRQTRDTEKDEFW  486
        mouse eEF-2K  449  -DLDDPEPREHG--HSNGNR-RHESDEDSLGS-SGRVCVETWNLLNPSRL  493

        human eEF-2K  495  ....A................EK....------------.I.........  532
   C.elegans eEF-2K  487  KVLRKQSVPANILSLQLQQMAANLENDEDVPQVTGHQFSVLGQIHIDLSR  536
        mouse eEF-2K  494  HLPRPSAVALEVQRLNALDLGRKIGK------------SVLGKVHLAMVR  531
```

Figure 2B

```
human eEF-2K       533  ..........G..----------------..Q...V.......N.....  565
C.elegans eEF-2K   537  YHELGRFVEVDSEHKEMLEGSENDARVPIKYDKQSAIFHLDIARKCGILE  586
mouse eEF-2K       532  YHEGGRFCEKDEE----------------WDRESAIFHLEHAADLGELE  564

human eEF-2K       566  ..........................------.....----------  596
C.elegans eEF-2K   587  AVLTSAHIVLGLPHELLKEVTVDDLFPNGFGEQENGIRADKGQKPCDLEE  636
mouse eEF-2K       565  AIVGLGLMYSQLPHHILADVSLKE-------TEENKTK----------  595

human eEF-2K       597  -..............Q..........S.Q..........L.........  645
C.elegans eEF-2K   637  FGSDLMEIAAEMGDKGAMLYMAHAYETGQHLGPNRRTDYKKSIDWYQRVV  686
mouse eEF-2K       596  -GFDYLLKAAEAGDRHSMILVARAFDTGLNLSPDRCQDWSEALHWYNTAL  644

human eEF-2K       646  -----.M......-.....M....R.MM........F...Y..E.D....  689
C.elegans eEF-2K   687  GFQEEEELDSDCGKTTFSSFAPLTRHEILAKMAEMYKEGGYGLNQDFERA  736
mouse eEF-2K       645  -----ETTDCDEG-GEYDGIQDEPQYALLAREAEMLLTGGFGLDKNPQRS  688

human eEF-2K       690  ..........................Q..........  725
C.elegans eEF-2K   737  YGLFNEAAEAAMEAMNGKLANKYYEKAEMC----GE  768
mouse eEF-2K       689  GDLYTQAAEAAMEAMKGRLANQYYEKAEEAWAQMEE  724
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Figure 2C

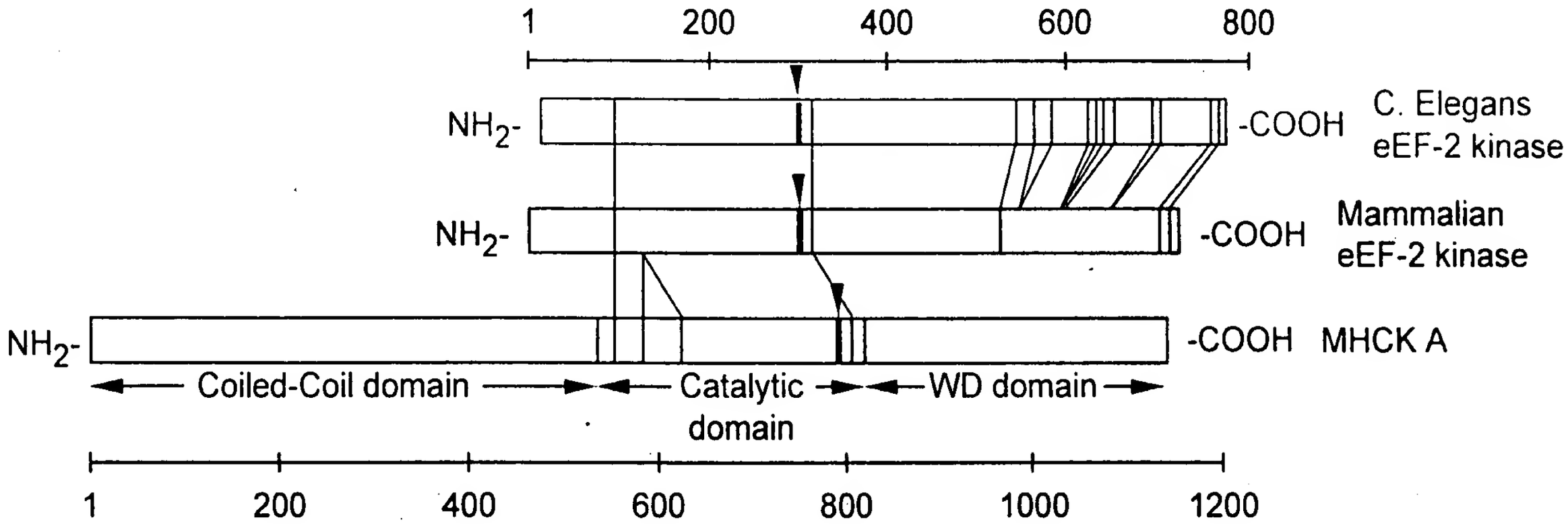
1
200
400
600
800
NH2-
-COOH
C. Elegans
eEF-2 kinase
NH2-
-COOH
Mammalian
eEF-2 kinase
NH2-
-COOH
MHCK A
Coiled-Coil domain
Catalytic
domain
WD domain
1
200
400
600
800
1000
1200

Figure 3

```
                      I                                                               II
H. EF-2K    124 WLDDEVLIKMASQPFGRGAMRECFRTKKLSNFLHAQ--------------------------QWKGASNYVAKRYIEPVD--------
C.e. EF-2K  110 WTEDIVDVRLHPDSFARGAMRECYRLKKCSKHGTSQ--------------------------DW--SSNYVAKRYICQVD--------
MHCK A      572 WIRLSMKLKVERKPFAEGALREAYHTVSLGVGTDENYPLGTTTKLFPPIEMISPISKNNEAMTQLKNGTKFVLKLYKKEAE--------
MHCK B      132 WTCTATLVKVEPVPFAEGAFRKAYHTLDLSKSGA----------------------------------SGRYVSKIGKK-----------
MhkC         48 WTHSIVCVSIEKTPFAKGSCRTAHKLKDWS--------------------------------QPDQGLVGKFSTNKK---------
Heart K     189 GDHLRGQISTEELHFGEGVHRKAFRSKVMQGLM--------------------------PVFQPGHACVLKVHNAVAHGTRNNDEL
Melanoma K   58 QLGLCAKIEFLSKEEMGGGLRRAVKVLCTWSEH--------------------------DILKSGHLYIIKSFLPEVINTWSSIYK
Ch 4 K     1027 AQETIVYLGDYLTVKKKGRQRNAFWVHHLHQEEIL-------------------------------GRYVGKDYKEQ----------
Consensus       *******o*o****F**G*oR*Ao****o****************************************oV*K*o************

                      III                          IV                          V
H. EF-2K    178 ----RDVYFEDVRLQMEAKLWGEEYNR----HKPPKQVDIMQMCIIELKDR----PGKPLF-HLEHYIEGKYIKYNSNSGFVRDDNI----
C.e. EF-2K  162 ----RRVLFDDVRLQMDAKLWAEEYNR----YNPPKKIDIVQMCVIEMIDV----KGSPLY-HLEHFIEGKYIKYNSNSGFVSNAA-----
MHCK A      653 QQASRELYFEDVKMQMVCRDWGNKFNQ----KKPPKKIEFLMSWVVELIDRSPSSNGQPILCSIEPLLVGEFKKNNSNYGAVLTN------
MHCK B      177 -PTPRPSYFEDVKMQMIAKKWADKYNS----FKPPKKIEFLQSCVLEFVDRTSSD----LICGAEPYVEGQYRKYNNNSGFVSNDE-----
MhkC         89 --TTRDSYFTDVLMQTFCAKWAEKFNE----AKPPKPITFLPSYVYELIDHPPPY---PV-CGGEPFIEGDYKKHNNNSGYVSSDA-----
Heart K     249 VQRNYKLAAQECYVQNTARYYAKIYAA----EAQPLEGFGEVPEIIPIFLIHRPENNIPY-ATVEEELIGEFVKYSIRDGKEINFLRRDSE
Melanoma K  118 EDTVLHLCLREIQQQRAAQKLTFAFNQ----MKP-KSIPYSP-RFLEVFLLYCHSAGQ-WFA-VEECMTGEFRKYNNNNGDEIIPTNTL--
Ch 4 K     1073 --KGLWHHFTDVERQMTAQHYVTEFNKRLYEQNIPTOIFYIPSTILLILEDKTI-KGC-I--SVEPYILGEFVKLSNNTKVVKTEYK----
Consensus       ******ooF*DV*oQ**A**o***oN*******PPK*I*oo***ooEoo**********o***oE*oo*G*o*KoN*N*G*V*********

                      VI                           VII                         VIII
H. EF-2K    252 -RLTPQAFSHFTFERSGHQLIVVDIQGVGD-------LYTDPQIHTET-----GTDFGDGNLGVRGMALFFY-SH-ACNRICESMGLAPF
C.e. EF-2K  235 -RLTPQAFSHFTFERSGHQMMVVDIQGVGD-------LYTDPQIHTVV-----GTDYGDGNLGTRGMALFFH-SH-RCNDICETMDLSNF
MHCK A      734 -RSTPQAFSHFTYELSNKQMIVVDIQGVDD-------LYTDPQIHTPD-----GKGFGLGNLGKAGINKFIT-TH-KCNAVCALLDL-DV
MHCK B      254 -RNTPQSFSHFTYEHSNHQLLIIDIQGVGD-------HYTDPQIHTYD-----GVGFGIGNLGQKGFEKFLD-TH-KCNAICQYLNLQSI
MhkC        165 -RNTPQSFSHFSYELSNHELLIVDIQGVND-------FYTDPQIHTKS-----GEGFGEGNLGETGFHKFLQ-TH-KCNPVCDFLKLKPI
Heart K     335 AGQKCCTFQHWVYQKTSGCLLVTDMQGVGM-------KLTDVGIATLAR---GYKGF-KGNCSMTFIDQFRA-LH-QCNKYCKMLGLKSL
Melanoma K  199 -EEIMLAFSHWTYEYTRGELLVLDLQGVGE-------NLTDPSVIKAEEKRSCDMVFGPANLGEDAIKNFRA-KH-HCNSCCRKLKLPDL
Ch 4 K     1153 ATEYGLAYGHFSYEFSNHRDVVVDLQGWVTGNGKGLIYLTDPQIHSVD-----QKVF-TTNFGKRGIFYFFNNQHVECNEICHRLSLTRP
Consensus       *******FSHF*YE*S***ooVoDoQGV*********ooTDPQIHT**********FG*GNLG**Go**Fo***H**CN*oC**L*L**o

                                                                                        Current Biology
```

Figure 4

```
   1 cgggcgcggg cgcgtccctc tggccagtca cccggcggag ctggtcgcac aattatgaaa
  61 gactcgactt ctgctgctag cgctggagct gagttagttc tgagaaggtt tcccggggct
 121 gtccttgttc ggtggcccgt gccaccgcct ccggagacgc tttccgatag gtggctgcag
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2821 atatttagga tttctgatgc tttatacatt tgtagttctt gtaaaaatgg aacagttacc
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```

Figure 5A

```
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5341 agttttcctg ttgtactgcc attcagcagg gcagtggttt gctgtagaag agtgcatgac
5401 tggtgaattt agaaaataca acaacaataa tggtgatgaa atcattccta caaatactct
5461 agaagagatc atgctagcct ttagccactg gacctatgaa tataccagag gggagttact
5521 ggtacttgac ttacaaggag tgggagaaaa cttgactgac ccatctgtaa taaaagctga
5581 agaaaaaaga tcctgtgaca tggtttttgg ccctgccaat ctaggagaag atgcaataaa
5641 aaacttcaga gccaaacatc actgtaattc ttgctgtcga aagcttaaac ttccagattt
5701 gaagaggaat gactacacgc ctgataaaat tatatttcct caggatgagt catcagattt
5761 gaatcttcaa tctggaaatt ccaccaaaga atcagaagca acaaattctg ttcgtctgat
5821 gttatagtgc tgagtcattg gtttttgcct acacttcaca aaagtgtaac tgtcagtttt
```

Figure 5B

```
5881 cctttcgggg gaattgatga tataggaaga tgtgtgcaaa atgagcttgc tggccccaca
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6001 aagtgctagc tggcagagag tcagtgctct cggctggtga agggcgggaa ccttgctgct
6061 gagagtggtg gttctctcac ctggtgcagg accattaacc aaagtcaagt cttcagattt
6121 gattggctgc tcagtcacag ccattcagct aaggaaacta aattgcgcag ctttttaaat
6181 ggctgaagtc ttcctcagtt tgtgctctat gataatgatg ttagctctca actaggtgtt
6241 tgtggccacg ggagaactac tccttacaat tttgcttcac aggcatgtta caaagcctgc
6301 actgaaaacc gtttgtcttc cctctctccc tccctctttt ccctgtagta ttgaggatca
6361 aacccagggc ctcatgaaga ccattttcta agagacattt tatttaagaa tcaactatag
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6481 ttttttaaca tttatcaatg ttaagtaaaa gaaagccatg ataaataaga attaactcac
6541 tgttcaatgg gtgtttcctg tgaggaaggt tacagttgta acagcctgca gttgcataca
6601 tctccaaaga tttacagact tagtgtatca aatcagagtg tcatgtgagc tctcacattg
6661 aaaattctat aggaatgtgt caatgtgaat tctatttctg gtacttaaga aatcagttgt
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6781 cttaattgcc cagatatttt tgcatattta gcaacaagaa aagcttatca tttgactcaa
6841 gttttatgct ttctctttct tttcatttcc taggtactaa ttttaatttt tatttggaag
6901 gagcagtgta aagcttactt gtattcaata gtgtatctca tagatacaga caaggccgca
6961 gagataagct gttaaatagt gtttaatgtt gatgtggaga gaaaggtgta ttacttaaaa
7021 atactatacc atatacgttt tgtatatcat taaatcttta aaagaaatta aatttattct
7081 tgtttacaaa
```


Figure 5C

MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTASLAM

KYSDVRLGEHFNQAIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEII

LQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKAAVTTGAWILTGGVNTGV

AKHVGDALKEHASRSSRKICTIGIAPWGVIENRNDLVGRDVVAPYQTLLNPLSKLNVLNN

LHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHARIGQGVPVVALIFEGGPNVILTV

LEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEGGNLPDAAEPDIISTIKKTFNFGQSE

AVHLFQTMMECMKKKELITVFHIGSEDHQDIDVAILTALLKGTNASAFDQLILTLAWDRV

DIAKNHVFVYGQQWLVGSLEQAMLDALVMDRVSFVKLLIENGVSMHKFLTIPRLEELYNT

KQGPTNPMLFHLIRDVKQGNLPPGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIYNSL

GGNNRRSGRNTSSSTPQLRKSHETFGNRADKKEKMRHNHFIKTAQPYRPKMDASMEEGKK

KRTKDEIVDIDDPETKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALVACKIYR

SMAYEAKQSDLVDDTSEELKQYSNDFGQLAVELLEQSFRQDETMAMKLLTYELKNWSNST

CLKLAVSSRLRPFVAHTCTQMLLSDMWMGRLNMRKNSWYKVILSILVPPAILMLEYKTKA

EMSHIPQSQDAHQMTMEDSENNFHNITEEIPMEVFKEVKILDSSDGKNEMEIHIKSKKLP

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VREVFMSEAGKISQKIKVWFSDYFNVSDTIAIISFFVGFGLRFGAKWNYINAYDNHVFVA

GRLIYCLNIIFWYVRLLDFLAVNQQAGPYVMMIGKMVANMFYIVVIMALVLLSFGVPRKA

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LFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYHFIMAYHEKPVLPPPLIILSHIVS

LFCCVCKRRKKDKTSDGPKLFLTEEDQKKLHDFEEQCVEMYFDEKDDKFNSGSEERIRVT

FERVEQMSIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQKASEASKV

HNEITRELSISKHLAQNLIDDVPVRPLWKKPSAVNTLSSSLPQGDRESNNPFLCNIFMKD

Figure 6A

EKDPQYNLFGQDLPVIPQRKEFNIPEAGSSCGALFPSAVSPPELRQRRHGVEMLKIFNKN

QKLGSSPNSSPHMSSPPTKFSVSTPSQPSCKSHLESTTKDQEPIFYKAAEGDNIEFGAFV

GHRDSMDLQRFKETSNKIRELLSNDTPENTLKHVGAAGYSECCKTSTSLHSVQAESCSRR

ASTEDSPEVDSKAALLPDWLRDRPSNREMPSEGGTLNGLASPFKPVLDTNYYYSAVERNN

LMRLSQSIPFVPVPPRGEPVTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGG

LRRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQ

KLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIPTN

TLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKAEEKRSCDMVFGPANLGEDA

IKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQDESSDLNLQSGNSTKESEATNSVR

LML

Figure 6B

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Figure 7A

MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTA
SLAMKYSDVKLGDHFNQAIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRL
SYDTKPEVILQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKAAVT
TGAWILTGGVNTGVAKHVGDALKEHASRSSRKICTIGIAPWGVIENRNDLVGRDVV
APYQTLLNPLSKLNVLNNLHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHAR
IGQGVPVVALIFEGGPNVILTVLEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEG
GNLPDAAEPDIISTIKKTFNFGQNEALHLFQTLMECMKRKELITVFHIGSDEHQDID
VAILTALLKGTNASAFDQLILTLAWDRVDIAKNHVFVYGQQWLVGSLEQAMLDAL
VMDRVAFVKLLIENGVSMHKFLTIPRLEELYNTKQGPTNPMLFHLVRDVKQGNLP
PGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIYNSLGGNNRRSGRNTSSSTPQLR
KSHESFGNRADKKEKMRHNHFIKTAQPYRPKIDTVMEEGKKKRTKDEIVDIDDPE
TKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALVACKIYRSMAYEAKQ
SDLVDDTSEELKQYSNDFGQLAVELLEQSFRQDETMAMKLLTYELKNWSNSTCLK
LAVAAKHRDFIAHTCSQMLLTDMWMGRLRMRKNPGLKVILSILVPPAILLLEYKT
KAEMSHIPQSQDAHQMTMDDSENNFQNITEEIPMEVFKEVRILDSNEGKNEMEIQM
KSKKLPITRKFYAFYHAPIVKFWFNTLAYLGFLMLYTFVVLVQMEQLPSVQEWIVI
AYIFTYAIEKVREIFMSEAGKVNQKIKVWFSDYFNISDTIAIISFFIGFGLRFGAKWNF
ANAYDNHVFVAGRLIYCLNIIFWYVRLLDFLAVNQQAGPYVMMIGKMVANMFYIV
VIMALVLLSFGVPRKAILYPHEAPSWTLAKDIVFHPYWMIFGEVYAYEIDVCANDS
VIPQICGPGTWLTPFLQAVYLFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYH
FIMAYHEKPVLPPPLIILSHIVSLFCCICKRRKKDKTSDGPKLFLTEEDQKKLHDFEE
QCVEMYFNEKDDKFHSGSEERIRVTFERVEQMCIQIKEVGDRVNYIKRSLQSLDSQI
GHLQDLSALTVDTLKTLTAQKASEASKVHNEITRELSISKHLAQNLIDDGPVRPSV
WKKHGVVNTLSSSLPQGDLESNNPFHCNILMKDDKDPQCNIFGQDLPAVPQRKEF
NFPEAGSSSGALFPSAVSPPELRQRLHGVELLKIFNKNQKLGSSSTSIPHLSSPPTKFF
VSTPSQPSCKSHLETGTKDQETVCSKATEGDNTEFGAFVGHRDSMDLQRFKETSN
KIKILSNNNTSENTLKRVSSLAGFTDCHRTSIPVHSKQEKISRRPSTEDTHEVDSKAA
LIPVWLQDRPSNREMPSEEGTLNGLTSPFKPAMDTNYYYSAVERNNLMRLSQSIPF
TPVPPRGEPVTVYRLEESSPNILNNSMSSWSQLGLCAKIEFLSKEEMGGGLRRAVK
VQCTWSEHDILKSGHLYIIKSFLPEVVNTWSSIYKEDTVLHLCLREIQQQRAAQKLT
FAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEF
RKYNNNNGDEIIPTNTLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKA
EEKRSCDMVFGPANLGEDAIKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQD
EPSDLNLQPGNSTKESESTNSVRLML

Figure 7B

GAATCTGCTGAGCCCCCACTAACCCAGAGTGATAAAAGAGAGACTTCTCACACCACAGCAGCAGCGACTGGTCGGAGTTCCCATGCTGATGCAAGAGAATGTGCTATTTCA
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TCCTGAAGGAAATGTCACAGACTTTTTGATAAGCCACAAAATGGAGGAACCTAAAATAGAGGTGCTTCAAATTGGGGAAACCAAACCCCCAAGCTCATCTAGCTCCTCAGCG
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GAGAAGTCCCTGGAAGCCCGAGCAGGCAAATCGCCAGGGACCCTCACAGCAGTGACGGGGTCAGAGGAGGTCAAGAGGAAGCCAGAAGCCCCAGGCAGTGGACATTTAGC
TGAGGGAGTAAAGAAGAAAATTTTGTCCAGGGTGGCAGCACTGAGGCTGAAACTGGAAGAAAAGGAAAATATCAGAAAGAACTCAGCCTTTCTTAAAAAGATGCCCAAACT
CGAAACATCATTATCACACACAGAAGAGAAACAAGACCCAAAAAAGCCATCTTGCAAAAGAGAAGGAAGAGCTCCAGTATTACTGAAAAAAATCCAAGCTGAGATGTTCCCT
GAACACTCTGGAAATGTAAAATTAAGCTGCCAATTTGCAGAAATTCATGAAGATTCTACTATCTGCTGGACAAAAGATTCAAAGTCCATAGCCCAAGTGCAGAGAAGTGCAG
GGGACAACTCCACTGTTTCCTTTGCCATCGTGCAAGCCAGTCCGAAGGACCAGGGACTCTATTACTGCTGCATCAAGAACAGCTACGGAAAAGTGACTGCTGAATTTAACCT
CACAGCTGAAGTTCTCAAACAGCTGTCAAGTCGCCAGGATACTAAAGGATGTGAAGAGATTGAATTCAGCCAACTCATCTTCAAAGAAGACTTCCTCCATGACAGCTACTTT
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CAAAATACTGCCAGGTATTATGCCAAGATCTACGCTGCTGAAGCACAGCCTCTGGAAGGCTTTGGAGAAGTACCTGAGATCATTCCTATTTTTCTTATCCATCGGCCTGAGA
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AGAAATGTTGCACCTTCCAGCACTGGGTGTACCAGAAAACAAGTGGCTGCCTCCTGGTGACGGACATGCAAGGTGTAGGAATGAAGCTAACTGACGTTGGCATAGCAACGC
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Figure 8A

ESAEPPLTQSDKRETSHTTAAATGRSSHADARECAISTQAEQEAKTLQTSTDSVSKEGNTNCKGEGMQVN
TLFETSQVPDWSDPPQVQVQETVRETISCSQMPAFSEPAGEESPFTGTTTISFSNLGGVHKENASLAQHSEV
KPCTCGPQQEEKQDRDGNIPDNFREDLKYEQSISEANDETMSPGVFSRHLPKDARADFREPVAVSVASPEP
TDTALTLENVCDEPRDREAVCAMECFEASDQGTCFDTIDSLVGTPVDNYSPQEICSVDTELAEGQNKVSD
LCSSNDKTLEVFFQTQVSETSVSTCKSSKDGNSVMSPLFISTFTLNISHTASEGATGENLAKVEKSTYPLAS
TVHAGQEQPSPSNSGGLDETQLLSSENNPLVQFKEGGDKSPSPSAADTTATPASYSSIVSFPWEKPTTLTAN
NECFQATRETVTIATEVHPAKYLAVSIPEDKHAGGTEERFPRASHEKVSQFPSQVQVDHILSGATIKSTKEL
LCRAPSVPGVPHHVLQLPEGEGFCSNSPLQVDNLSGDKSQTVDRADFRSYEENFQERGSETKQGVQQQSL
SQQGSLSAPDFQQSLPTTSAAQEERNLVPTAPSPASSREGAGQRSGWGTRVSVVAETAGEEDSQALSNVPS
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QPSIGKSKVQTNSMTVKKAGPETPGEKKT

Figure 8B

```
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121   aggtgttact gtggccgact gattggagac catgctggga tagattattc ctggaccatc
181   tcagctgcca agggtaaaga aagtgaacaa tggtctgttg aaaagcacac aacgaaaagc
241   ccaacagata cttttggcac gattaatttc caagatggag agcacaccca tcatgccaag
301   tatattagaa cttcttatga tacaaaactg gatcatctgt tacatttaat gttgaaagag
361   tggaaaatgg aactgcccaa gcttgtgatc tcagtccatg ggggcatcca gaactttact
421   atgccctcta aatttaaaga gattttcagc caaggtttgg ttaaagctgc agagacaaca
481   ggagcgtgga taataactga aggcatcaat acagtgtcca agcatgttgg ggatgccttg
541   aaatcccatt cctctcattc cttgagaaaa atctggacag ttggaatccc tccttggggt
601   gtcattgaga accagagaga ccttattgga aaagatgtgg tgtgcctgta ccagactctg
661   gataaccccc tcagcaagct cacaacactc aacagcatgc actcgcactt catcctgtct
721   gatgatggga ccgtgggcaa gtatggaaat gaaatgaagc tcagaaggaa cctggagaag
781   tacctctctc tgcagaaaat acactgccgc tcaagacaag gcgtgccggt cgtggggctg
841   gtggtggaag gcggtcccaa cgtcatcctg tcagtgtggg agactgtcaa ggacaaggac
901   ccagtggtgg tgtgtgaggg cacaggtagg gcggctgacc tcctggcctt cacacacaaa
961   cacctggcag atgaagggat gctgcgacct caggtgaaag aggagatcat ctgcatgatt
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1141  ctggacttag caatcctaac agctttgctg aagggcacaa atttatcagc gtcagagcaa
1201  ttaaatctgg caatggcttg ggacagggtg gacattgcca agaaacatat cctaatttat
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1321  cgggtggatt ttgtgaagct cttaatagaa tatggagtga acctccatcg ctttcttacc
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1441  catctcgtcc aagatgtgaa acagcatacc cttctttcag gctaccgaat aaccttgatt
1501  gacattggat tagtagtaga atacctcatt ggtagagcat atcgcagcaa ctacactaga
1561  aaacatttca gagccctcta caacaacctc tacagaaaat acaagcacca gagacactcc
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1681  cagccataca aattcaagga aaagtctata gtccttcata aatcaaggaa gaagtcaaaa
1741  gaacaaaatg tatcagatga ccctgagtct actggctttc tttaccctta caatgacctg
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2041  atgacgctgt tgacgtatga actcaggaac tggagcaatt cgacctgcct taaactggcc
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2401  gaaaatcagc attttggttt ggaaagtggg caccaacacc ttccgtggac caggaaagtc
2461  tatgagttct acagtgctcc aattgtcaag ttttggtttt atacgatggc gtatttggca
2521  ttcctcatgc tgttcactta caccgtgttg gtggagatgc agccccagcc cagcgtgcag
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2821  cggctcctgg acttctttgc tgtgaatcaa catgcaggtc catatgtgac catgattgca
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3001  gatattgtat ttgagccata ctggatgata tacggagaag tctatgctgg agaaatagat
3061  gtttgttcaa gccagccatc ctgccctcct ggttcttttc ttactccatt cttgcaagct
3121  gtctacctct tcgtgcaata tatcatcatg gtgaacctgt tgattgcttt cttcaacaac
3181  gtttacttag atatggaatc catttcaaat aacctgtgga aatacaaccg ctatcgctac
```

Figure 9A

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3361 gttggattaa aactctacct cagtaaggag gatctgaaaa aacttcatga ttttgaggag
3421 cagtgcgtgg aaaaatactt ccatgagaag atggaagatg tgaattgtag ttgtgaggaa
3481 cgaatccgag tgacatcaga aagggttaca gagatgtact tccagctgaa agaaatgaat
3541 gaaaaggtgt cttttataaa ggactcctta ctgtctttgg acagccaggt gggacacctg
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3661 caagaggatg aggctctcct ggccaagaga aagcattcta cttgcaaaaa acttccccac
3721 agctggagca atgtcatctg tgcagaggtt ctaggcagca tggagatcgc tggagagaag
3781 aaataccagt attatagcat gccctcttct ttgctgagga gcctggctgg aggccggcat
3841 cccccaagag tgcagagggg ggcacttctt gagattacaa acagtaaaag agaggctaca
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3961 tctcctaaca ggcaagcaca ctcaaagtat ggccagtttc ttctggtccc ctctaatcta
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6241 agctccatcc tcaagttcca cacgaagatg cttggatgag tcagctggga atattgttct
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6361 aggatggggt tgggggggat acatttattt tattttctca ctatgtatgc agactggacc
6421 ccctactact atttgtcacc tcacccacag attgtattta tgtctatata tatgttcata

Figure 9A

6481 aaaagttatg tgatttcctc ctctgtcttt tccacaacat aggactttga atagcaatga
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6601 taccaagtat actggtgaaa tctcgatggg tttcagatat tgtcagtgaa tcatatgatg
6661 cctggatatt tcaggtttct gtaaaagaaa gggaaaccta aaacaaatac ccttccatat
6721 ataatatata tggaatatgt atattatata tatttttata tatataatat atatggaata
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6841 tttatttttg agatggagtt tcactctttt tacccaggct ggagtgcaat gatgcgatct
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7321 gaaagatacg gtttcagact gaaaacatgt ttcacaggtg tttgcttcct tccagagcag
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Figure 9A

MSQKSWIKGVFDKRECSTIIPSSKNPHRCTPVCQVCQNLIRCYCGRLIGDHAGIDYS
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NSCCRKLKLPDLKRNDYSPERINSTFGLEIKIESAEEPPARETGRNSPEDDMQL

Figure 9B

GTATCAGGACTCAGCCCATTTCCCCCTCTGGTGCTGAGAAATGGAGGCCGAAGGAGTGATCTAGAAGTGTTAATTGAGCCCCTAATCTATGCTAGTTAC
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CTGCAGACACCAGGGCCGCCAAGGGAGCGGACTCGGAGCCGGCCCTGGGGCGGGCACATGGGCCCCGGCGCCCCCCGGCGTCTCCAAGCCGCGCTGC
CCGGGTCGGGCCAGGCCAGGGGAGGGACAGCAGCAGGTGACGACGGCCCGGCCACCGGCTATAAATAGGGGCGCGCGTCAGCCGCGGGCGGGAGCG
GCGGCGGCGGGCAGGGGCCCGGGGGCCGGGGCCTGGAGGACAGGCGAGGCAGCGGCGAGTGCGGGGCCGGCGGTCGGGGAGGGCGGTGCCATGGG
GTCGCGGAGGGCCCCCACCCGGGGCTGGGGCGCGGGTGGGCGGTCGGGGGCGGGGGGCGACGGTGAGGACGACGGCCCCGTGTGGATCCCCAGCCC
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CACAGGATACCCAGAGCCAGAGGTGACCTGGTACAAGGATGATACGGAGCTGGACCGCTACTGTGGCTTGCCAAAATATGAGATCACTCATCAGGGCA
ACCGCCACACACTGCAGCTGTACAGGTGTCGAGAAGAAGATGCCGCCATCTACCAGGCCTCTGCCCAGAACAGCAAGGGCATTGTGTCCTGCTCAGGG
GTCCTGGAGGTGGGCACCATGACTGAGTACAAGATCCACCAGCGCTGGTTCGCCAAGTTGAAGCGCAAGGCTGCGGCAAAGCTGCGCGAGATCGAGCA
GAGCTGGAAGCACGAGAAGGCGGTGCCTGGGGAGGTCGACACTCTGCGCAAGCTCAGCCCCGACCGCTTCCAGCGAAAGCGGCGATTGAGCGGGGCT
CAAGCGCCGGGCCCCTCGGTCCCTACCAGGGAGCCTGAGGGTGGGACCCTGGCGGCTTGGCAGGAGGGAGAGACTGAGACTGCTCAGCACTCAGGTT
TGGGCCTGATCAACAGTTTTGCTTCTGGAGAAGTGACCACCAACGGGGAGGCTGCCCCCGAGAATGGAGAGGACGGAGAGCATGGCTTGCTGACATAC
ATCTGTGACGCCATGGAGCTGGGGCCTCAGAGAGCCCTCAAAGAGGAGAGTGGGGCCAAGAAGAAAAAGAAAGATGAGGAATCCAAGCAAGGCCTGC
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GTGGGCGTGGAGCAGGTTCAGACCCAGCCCAGAGGCAGGGCTGCACGGGGGCCTGGGTCCTCTGGCACAGATAGTACCAGGAAGCCAGCCTCTGCTG
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Figure 10A

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TCAGTCTTGACATGGGCCAAGGATCAGCGCCCAGTGGGCGAGGTGGGCAGGAGCGCAGGGGATGAGGGGCCGGCGGCCTTGGCCATCGTGCAGGCCT
CCCCCGTAGACTGCGGTGTGTATCGGTGCACCATCCACAATGAGCACGGCTCGGCCTCCACCGACTTCTGCCTCAGCCCTGAGGTGTTGTCAGGATTCA
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CTTCGAGTCGGGCCGCACGTGCATCATCAAGGTGTCCAGCCTGCTTGTGTTTGGGCCCAGCAGTGAGACTTCTCTTGTGGGCAGAAACTACGACGTCAC
CATCCAGGGGTGCAAGATCCAGAACATGAGTCGGGAGTACTGCAAAATCTTCGCAGCAGAAGCCCGGGCCGCGCCTGGCTTTGGGGAGGTGCCTGAGA
TCATCCCACTGTATCTGATCTACCGGCCTGCAAACAATATCCCATATGCTACCCTGGAGGAAGACCTGGGCAAGCCCCTGGAGTCTTACTGTTCTCGGG
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GGGCACCCGGAAGAGTGCTCCAAGTTCCAAGGCCACCCCTCAGGCCTCAGAGCCAGTCACCACTCAGTTGTTGGGACAGCCTCCCACCCAAGAGGAGG
GCTCCAAGGCCCAGGGCATGCGGTAGCCTCTGCAGAGGCTGGGGGCCTCCACCCAGCAGCAGACCAACCAGGAAGCAGCTTGAACTGGATGGAGACTT
TCCAAATATGGAACTAACTGGAGAAGGTGCACGAAGGAGACACCACTTGGGGACCTCTCTGAGCAGGCTCTCGTGAATCAGCTCGTCATCAGATGGCTT
TGGTGCATGGCACATAGCCCACTGGCCTCTTCTGGTGCCACTGTCACCCAGGGCTCCCGGGCCTCAAGCAGTCCCCACCTCCGAGTGCCTGGCAACCTA
GGCCCTCCTTGAAGTTTACACTTTGCCACTGCTGGAGGCTCCCCTGAGTCCTCTGCATGAGTTCTGCACCCCAAGCCCTTGCCCCAGCCCAGTCCAGCA
GCAGATGTTACAATCTGAGTGAGGACATGCAGGCCAACTTTTACCCTCCTGCATTTGCCTGGCCCTGATCTCGCCTGTCCTCAGGGATCCAGACTTCCTC
TGCTGGTCTGGCCTGGTGACTCTCAGGGTATCTTCTCCTTCCAGCTACTTTCGCTCACTGATCTCAGCTTATCCTGCAACTAACCATCCTTGAGCCCAGA
TGGGGCTCAGGGCCCTTCCAGAGCCTGTCATGTCCTTGTGCAGTGGCCTTTGATGTGTGTTCACGCTCTTCCCCCTTCACTCACTCGCCTGCTTCCCATG
CTCCCTTGTACCCCCTCGCCACATCCCTGTCTTGGGGCCCAGCTGCAGCCTGCTGCCTGCCCTTCATGGCTCTGCACATGGCCCTTTGCTTGAGGGCTC
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TGCCTCTCAGCTACTTGCTGACCATTTCCTGCTTCTCAAGCTGCAGAGAAGCTTTTCATTCCCACCCCCACCCGGAACCTCCCCTTGCCTAACATTTCCC
CTCTATGGTAACATCTCTGACTTCTCTACCTCCTCTGTGCTCAGGTGACTCCACATCTTCTGCCCCAGTGTGTCCCCACCTCTCCCAGCCTGTATACCCA
GATTACTTTGGTGAACTGAAAAA

Figure 10A

MEVAWLVYVLGQQPLARQGEGQSRLVPGRGLVLWLPGLPRSSPSWPAVDLAPLAPARPRGPLICHTGHEQAGREPG
PGSSTKGPVLHDQDTRCAFLPRPPGPLQTRRYCRHQGRQGSGLGAGPGAGTWAPAPPGVSKPRCPGRARPGEGQQQ
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EATTDSKPISSLSQAPECGAQSLGKAPPQASVQVPTPPARRRHGTRDSTLQGQAGHRTPGEVLECQTTTAPTMSASSSS
DVASIGVSTSGSQGIIEPMDMETQEDGRTSANQRTGSKKNVQADGKIQVDGRTRGDGTQTAQRTRADRKTQVDAGT
QESKRPQSDRSAQKGMMTQGRAETQLETTQAGEKIQEDRKAQADKGTQEDRRMQGEKGMQGEKGTQSEGSAPTA
MEGQSEQEVATSLGPPSRTPKLPPTAGPRAPLNIECFVQTPEGSCFPKKPGCLPRSEEAVVTASRNHEQTVLGPLSGNL
MLPAQPPHEGSVEQVGGERCRGPQSSGPVEAKQEDSPFQCPKEERPGGVPCMDQGGCPLAGLSQEVPTMPSLPGTG
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DPGLIDSLKNYLLLLLKLSSTETSGAGGESQVGAATGGLVPSATLTPTVEVAGLSPRTSRRILERVENNHLVQSAQTLL
LSPCTSRRLTGLLDREVQAGRQALAAARGSWGPGPSSLTVPAIVVDEEDPGLASEGASEGEGEVSLEGPGLLGASQES
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GVYRCTIHNEHGSASTDFCLSPEVLSGFISREEGEVGEEIEMTPMVFAKGLADSGCWGDKLFGRLVSEELRGGGYGC
GLRKASQAKVIYGLEPIFESGRTCIIKVSSLLVFGPSSETSLVGRNYDVTIQGCKIQNMSREYCKIFAAEARAAPGFGEV
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Figure 10B

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GAATATGGCTTGGCCTATGGCCATTTTTCTTATGAGTTTTCTAATCATAGAGATGTTGTGGTCGATTTACAAGGTTGGGTAACCGGTAATGGAAAAGGAC
TCATCTACCTCACAGATCCCCAGATTCACTCCGTTGATCAGAAAGTTTTCACTACCAATTTTGGAAAGAGAGGAATTTTTTACTTCTTTAATAACCAGCAT
GTGGAATGTAATGAAATCTGCCATCGTCTTTCTTTGACTAGACCTTCAATGGAGAAACCA

Figure 11A

MNNQKVVAVLLQECKQVLDQLLLEAPDVSEEDKSEDQRCRALLPSELRTLIQEAKEMKWPFVPEK
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KGLHKLQPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNGATGTWLYRNESDKVLVQSVCIQI
RGQILQKLGMWYEAAELIWASIVGYLALPQPDKKGLSTSLGILADIFVSMSKNDYEKFKNNPQINLS
LLKEFDHHLLSAAEACKLAAAFSAYTPLFVLTAVNIRGTCLLSYSSSNDCPPELKNLHLCEAKEAFEI
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DREALSQEVMSVIAQVKEHLQVQSFSNVDDRSYVPESFECRLDKLILHGQGDFQKILDTYSQHHTSV
CEVFESDCGNNKNEQKDAKTGVCITALKTEIKNIDTVSTTQEKPHCQRDTGISSSLMGKNVQRELRR
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LGEFVKLSNNTKVVKTEYKATEYGLAYGHFSYEFSNHRDVVVDLQGWVTGNGKGLIYLTDPQIHSV
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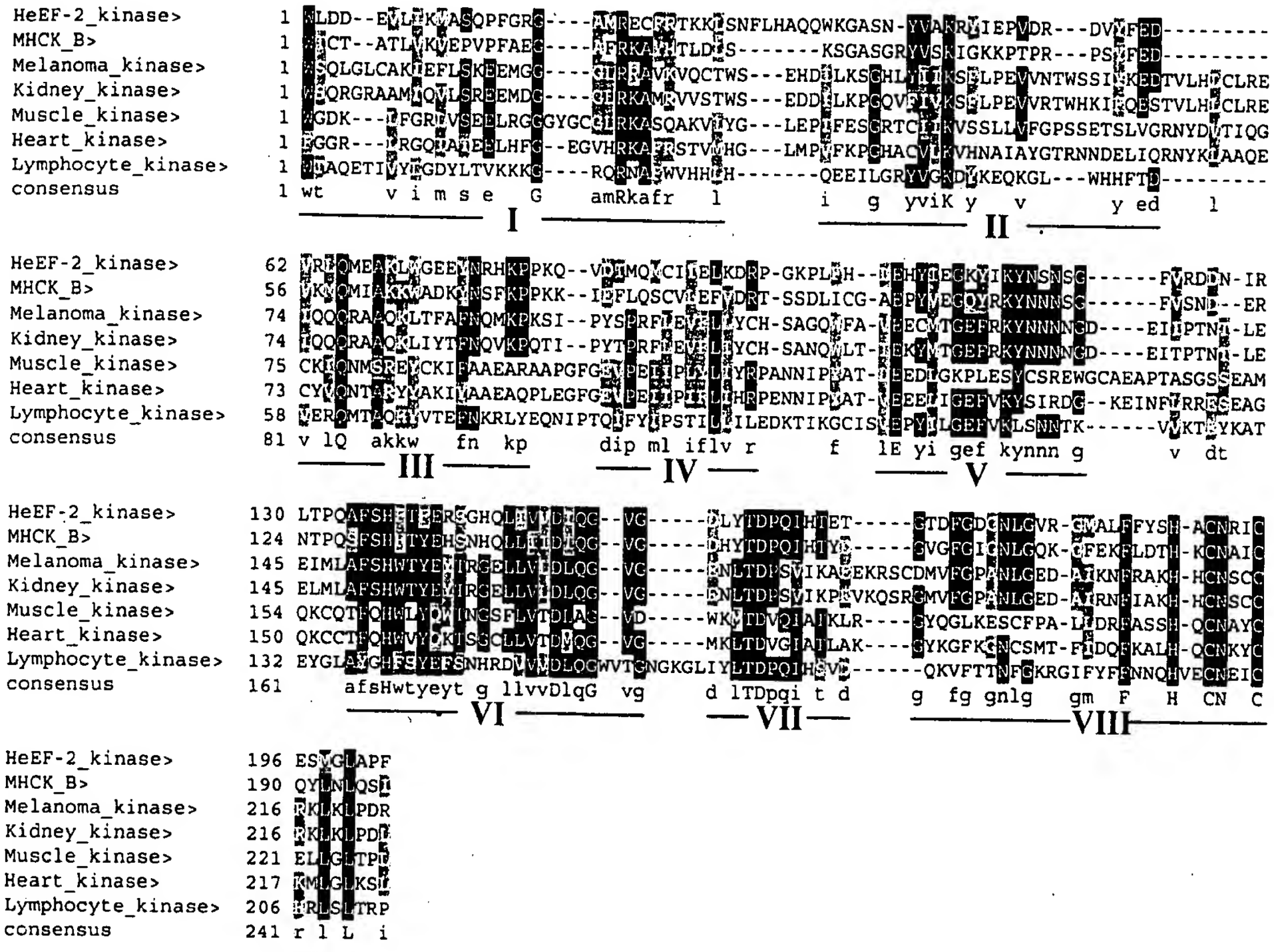
Figure 11B

A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MHCK_B>
Melanoma_kinase>
Kidney_kinase>
Muscle_kinase>
Heart_kinase>
Lymphocyte_kinase>
consensus
I
II
III
IV
V
VI
VII
VIII

Figure 12

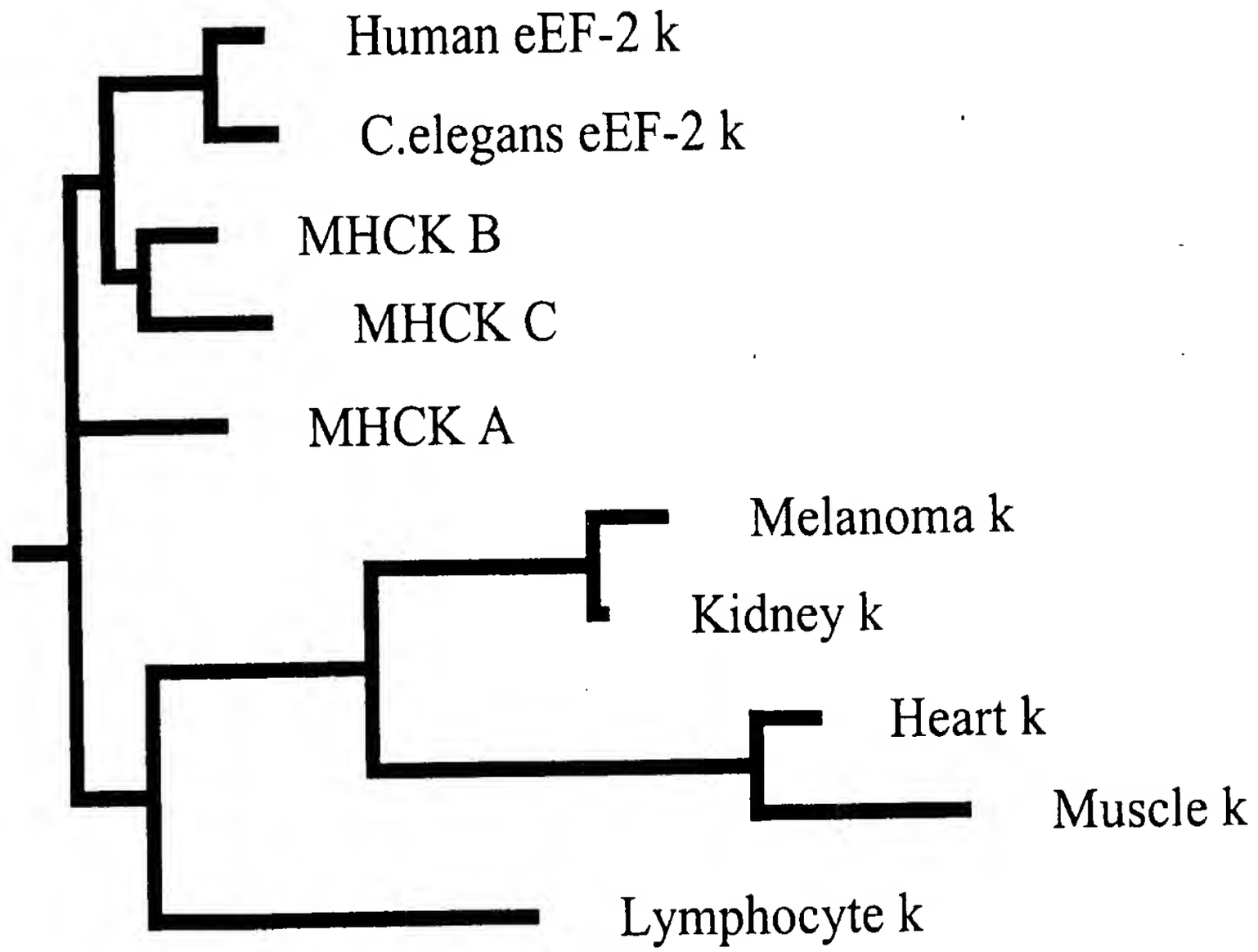
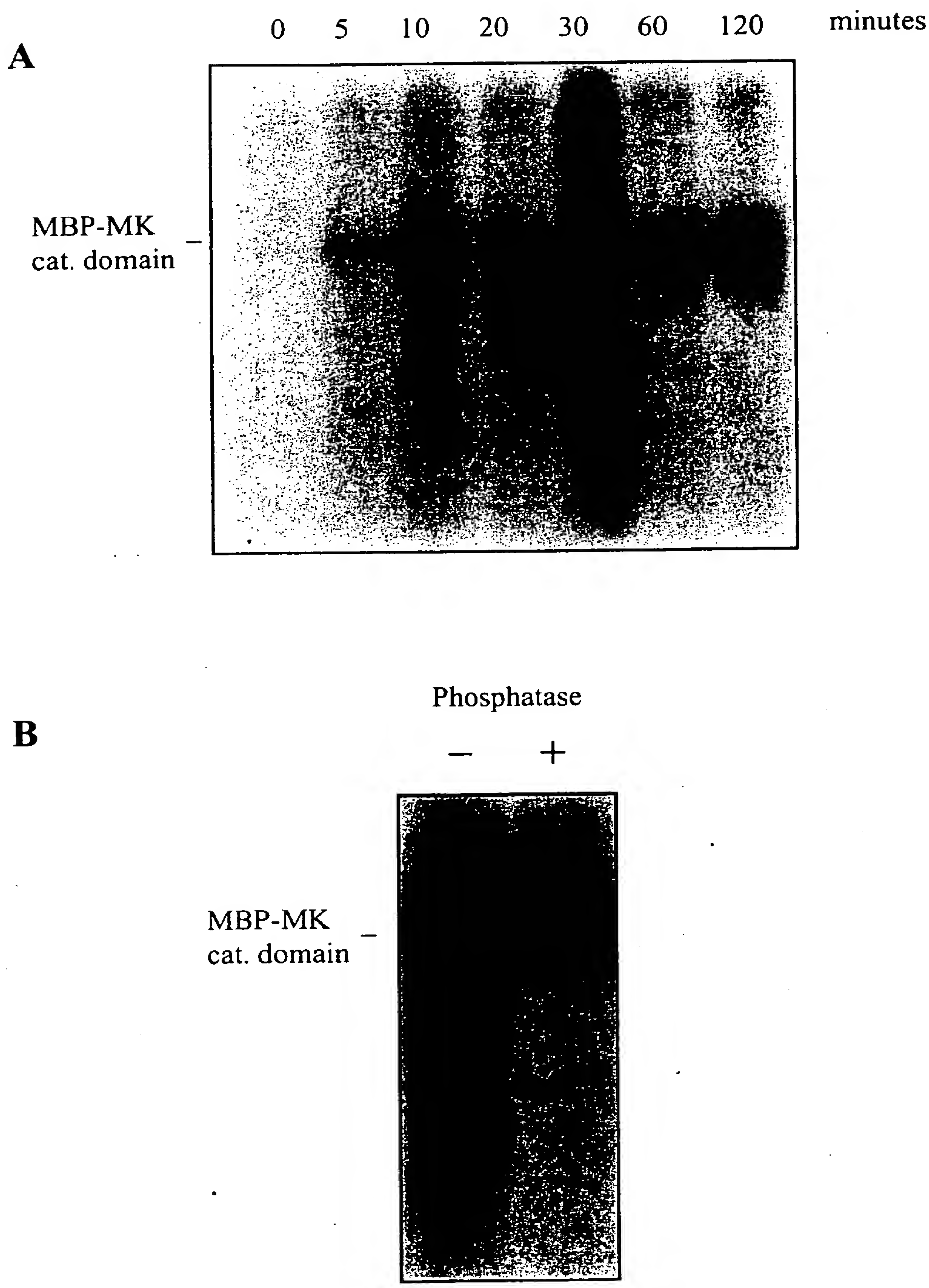


Fig. 1

Figure 13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30
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minutes
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B
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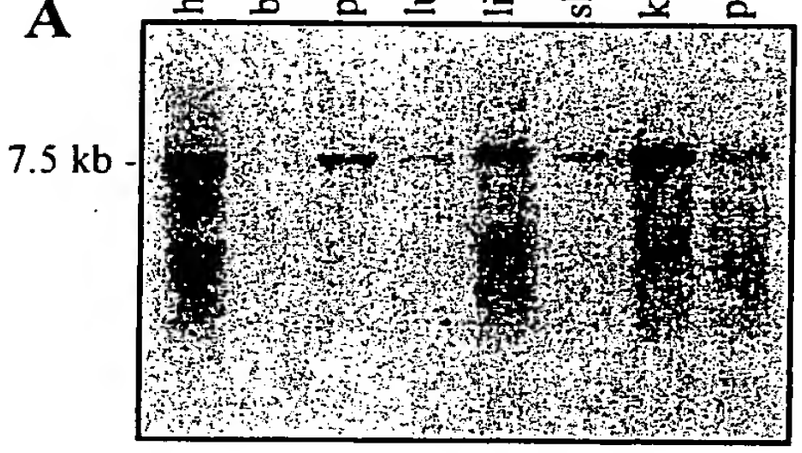
MBP-MK cat. domain

Figure 14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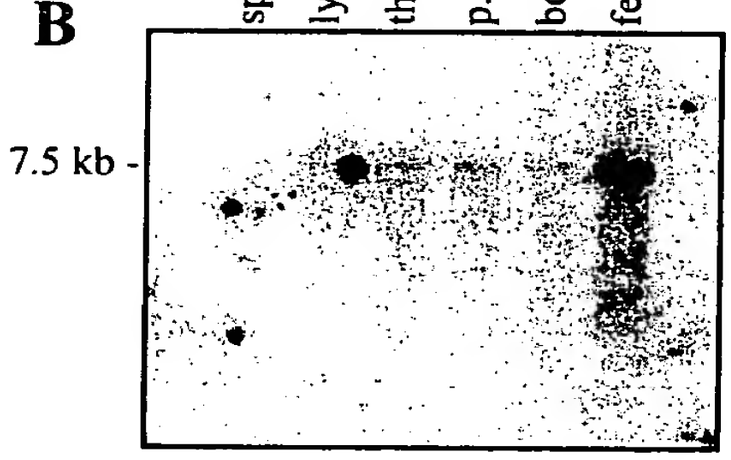
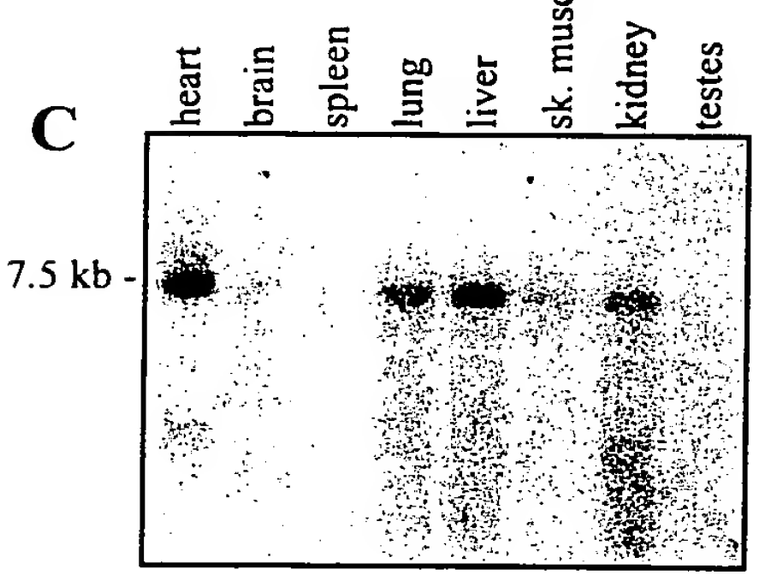
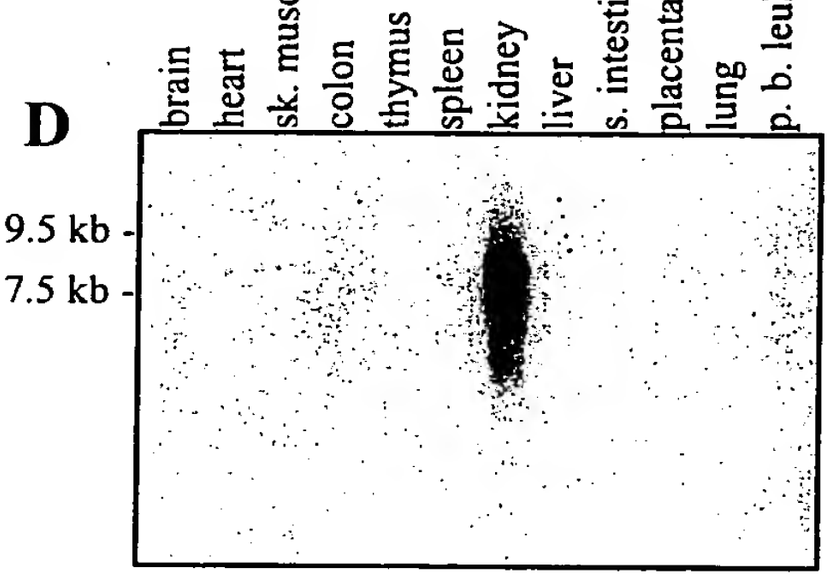
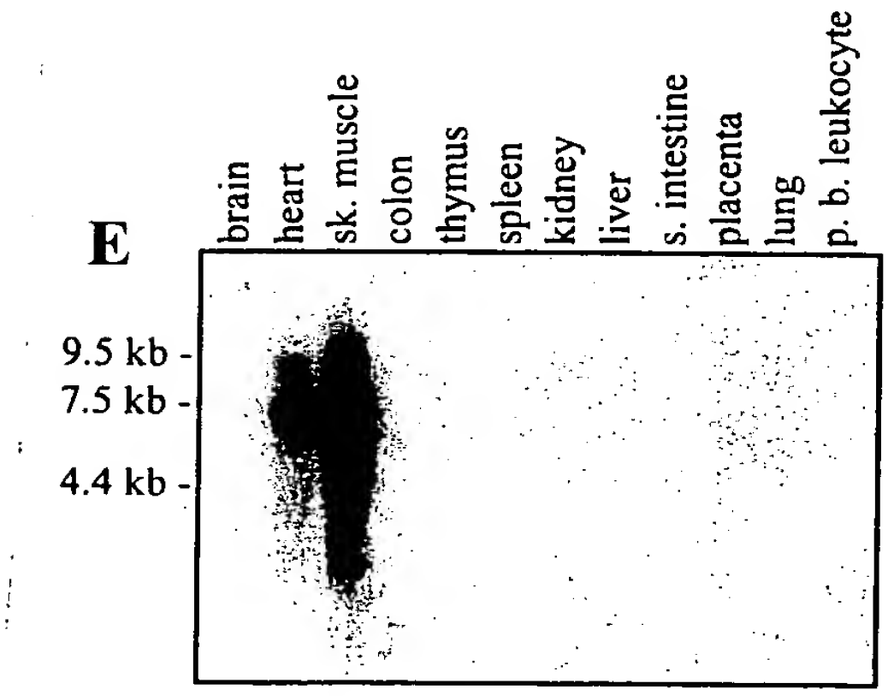
heart
brain
placenta
lung
liver
sk. muscle
kidney
pancreas
7.5 kb -


B
spleen
lymph node
thymus
p. b. leukocyte
bone marrow
fetal liver
7.5 kb -


C
heart
brain
spleen
lung
liver
sk. muscle
kidney
testes
7.5 kb -


D
brain
heart
sk. muscle
colon
thymus
spleen
kidney
liver
s. intestine
placenta
lung
p. b. leukocyte
9.5 kb -
7.5 kb -


E
brain
heart
sk. muscle
colon
thymus
spleen
kidney
liver
s. intestine
placenta
lung
p. b. leukocyte
9.5 kb -
7.5 kb -
4.4 kb -

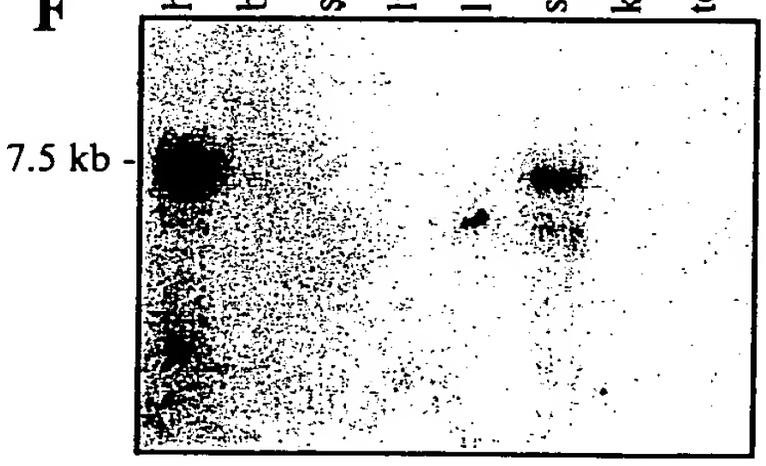

F
heart
brain
spleen
lung
liver
sk. muscle
kidney
testes
7.5 kb -

Figure 15

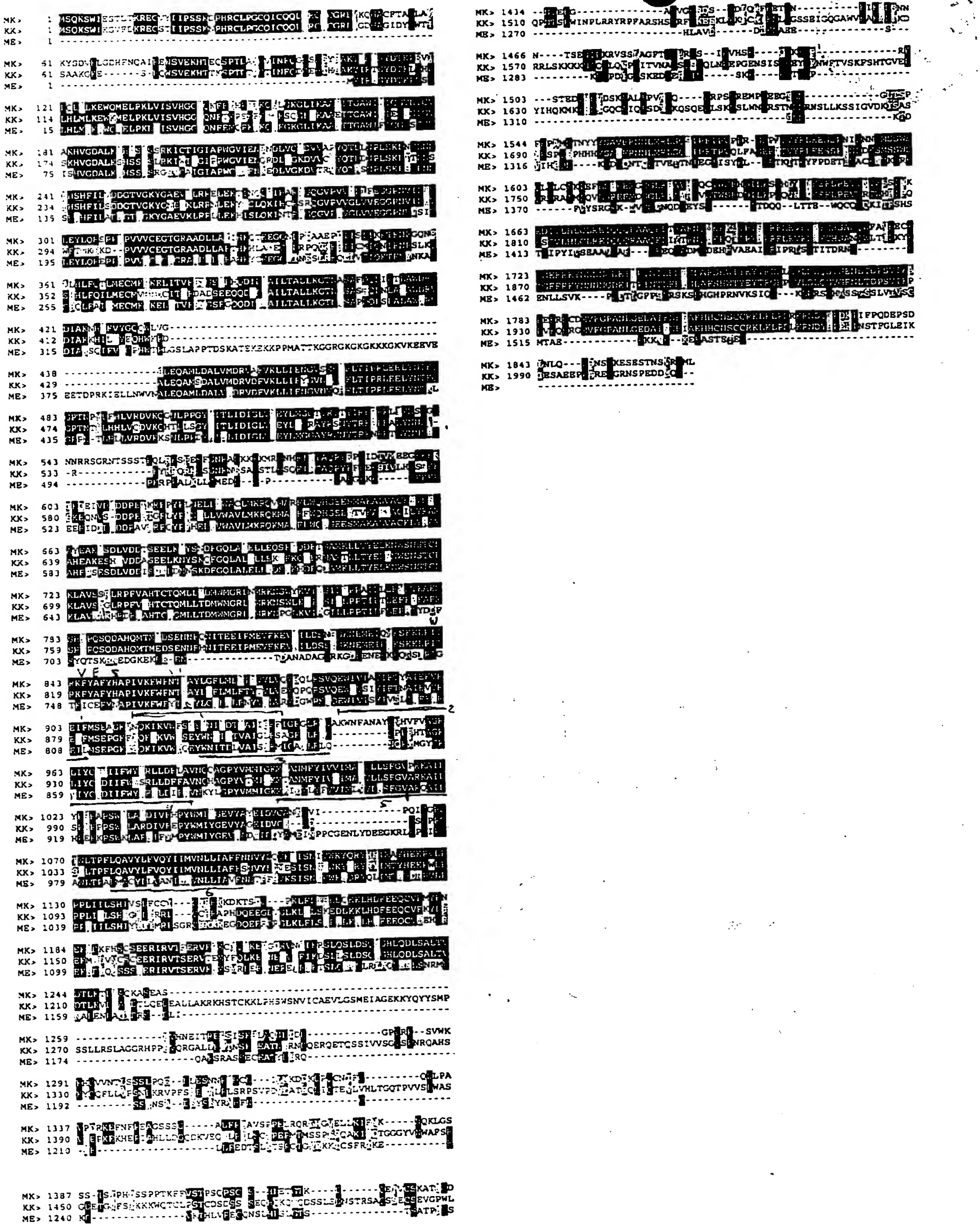


Figure 16

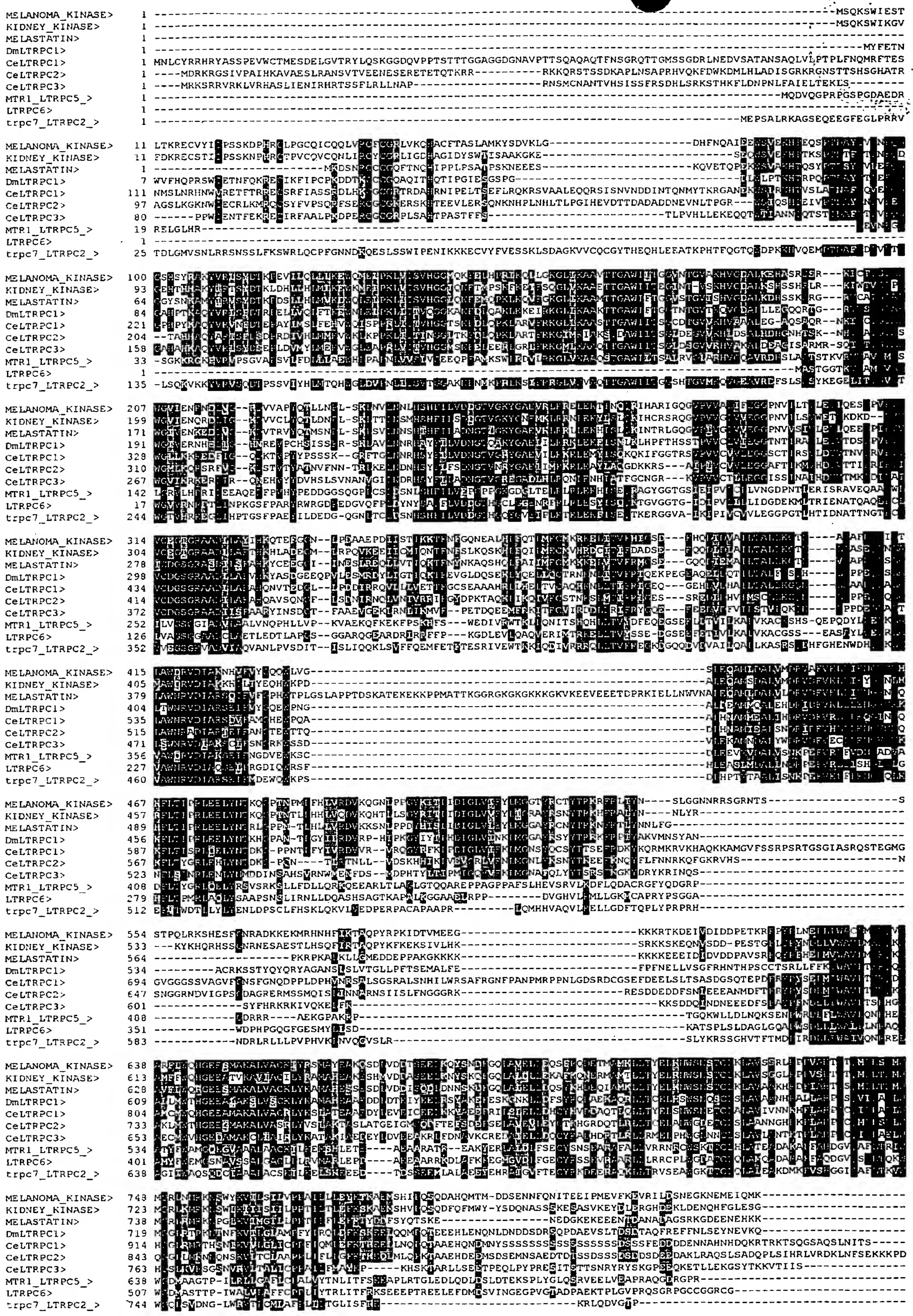

MELANOMA_KINASE>
KIDNEY_KINASE>
MELASTATIN>
DmLTRPC1>
CeLTRPC1>
CeLTRPC2>
CeLTRPC3>
MTR1_LTRPC5_>
LTRPC6>
trpc7_LTRPC2_>

Figure 17A

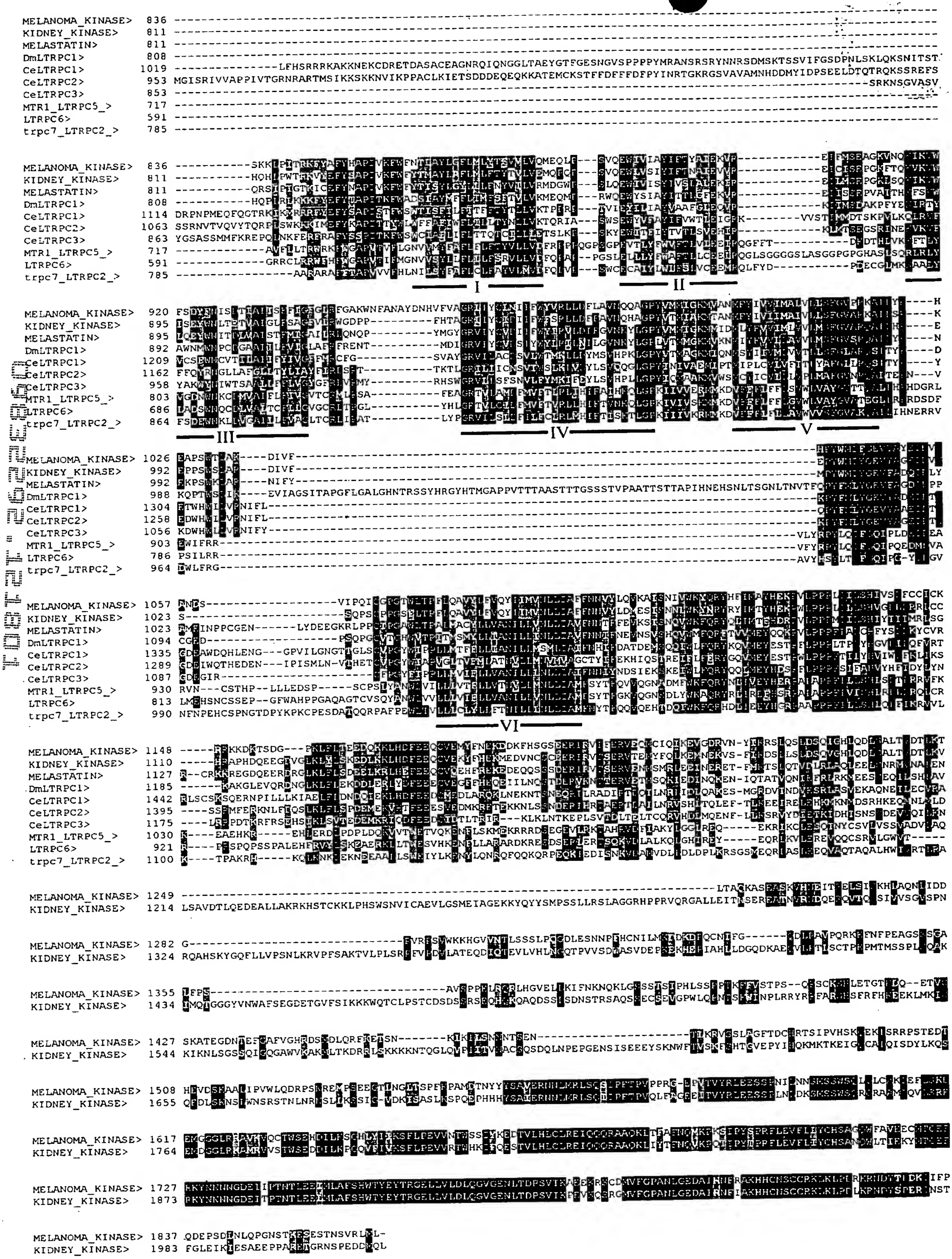

MELANOMA_KINASE>
KIDNEY_KINASE>
MELASTATIN>
DmLTRPC1>
CeLTRPC1>
CeLTRPC2>
CeLTRPC3>
MTR1_LTRPC5_>
LTRPC6>
trpc7_LTRPC2_>
I
II
III
IV
V
VI

Figure 17B

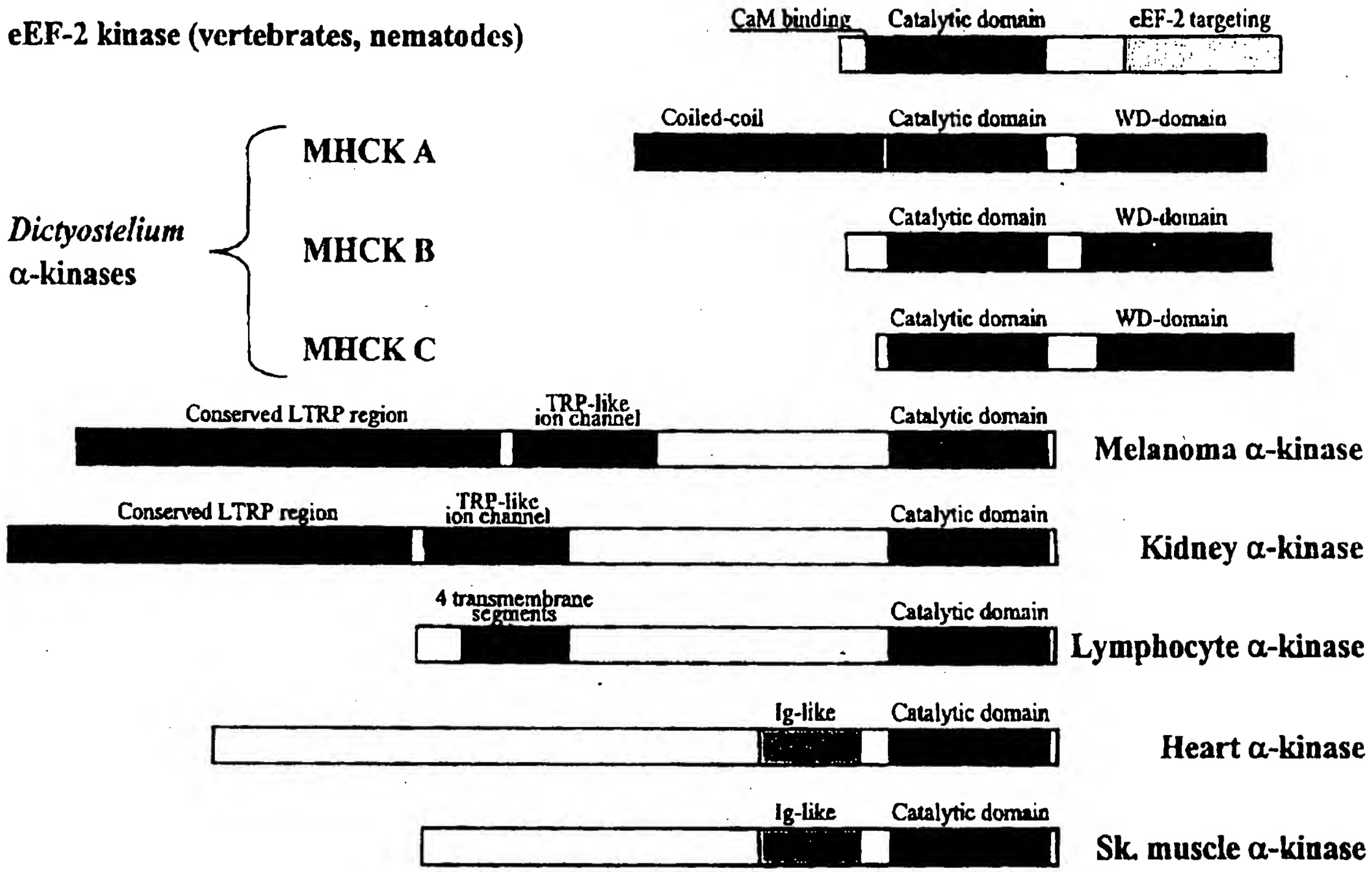
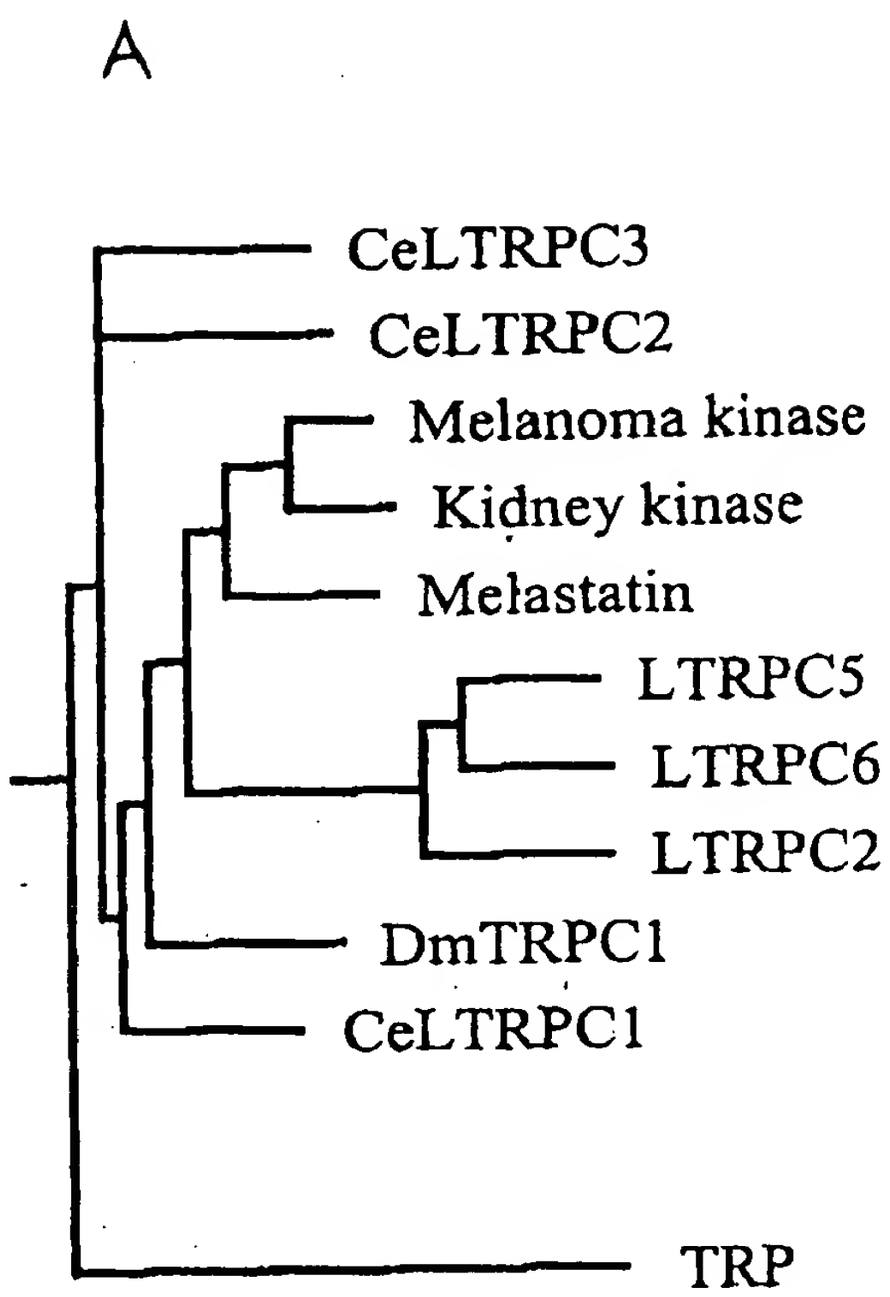

eEF-2 kinase (vertebrates, nematodes)
CaM binding
Catalytic domain
eEF-2 targeting
Dictyostelium α-kinases
MHCK A
Coiled-coil
Catalytic domain
WD-domain
MHCK B
Catalytic domain
WD-domain
MHCK C
Catalytic domain
WD-domain
Conserved LTRP region
TRP-like ion channel
Catalytic domain
Melanoma α-kinase
Conserved LTRP region
TRP-like ion channel
Catalytic domain
Kidney α-kinase
4 transmembrane segments
Catalytic domain
Lymphocyte α-kinase
Ig-like
Catalytic domain
Heart α-kinase
Ig-like
Catalytic domain
Sk. muscle α-kinase

Figure 18



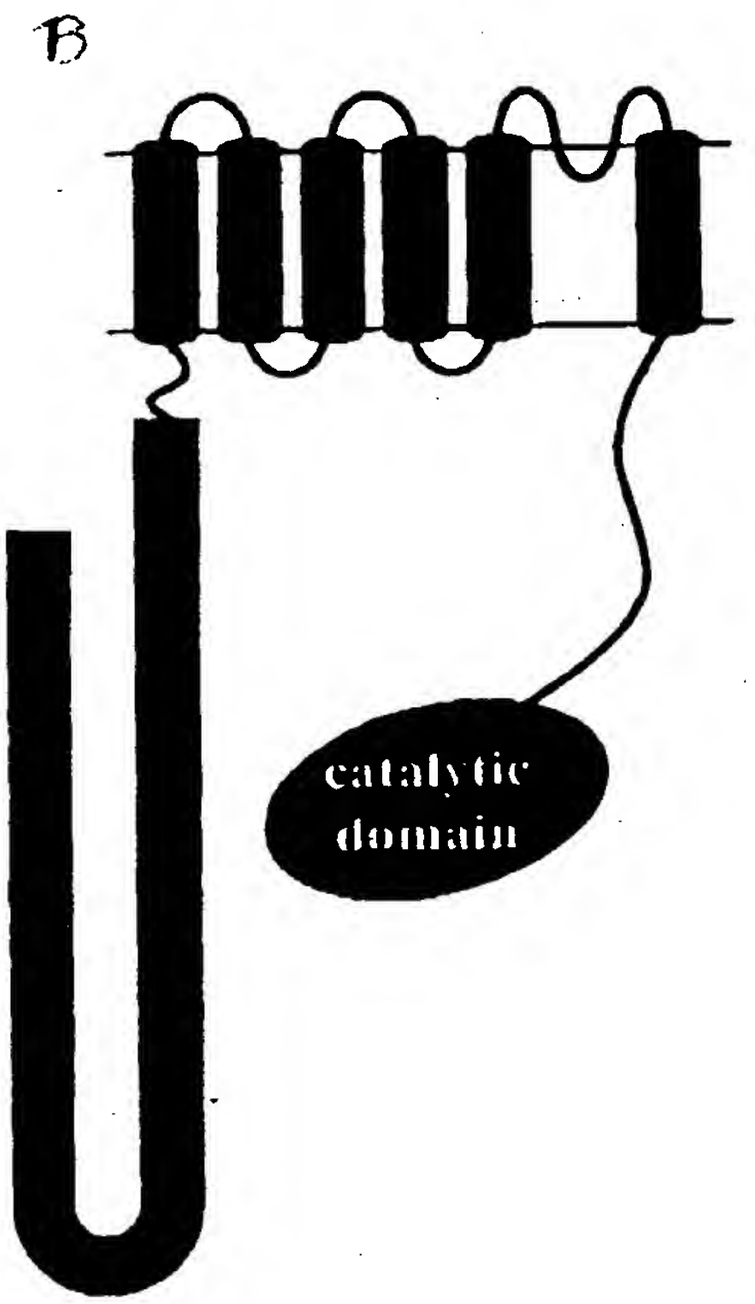


Figure 19